

Patient Name SAMPLEREPORT,SDEL	Patient ID SA00056048	Age 49	Gender F	Order # SA00056048
Ordering Phys CLIENT,CLIENT				DOB 08/09/1963
Client Order # SA00056048	Account Information			Report Notes
Collected 03/21/2013 13:50	C7028846-DLMP Rochester 3050 Superior Drive Rochester, MN 55901			
Printed 04/16/2013 15:12				

Test	Flag	Results	Unit	Reference Value	Perform Site*
Single-gene Large Del/Dup			REPORTED	03/26/2013 14:07	
Reason for Referral		Family history of Li-Fraumeni syndrome. Test for the presence of a familial large deletion/duplication in the TP53 gene.			MCR
Result		The following deletion was detected: Exon(s): 1-11 Classification: DELETERIOUS			MCR
Interpretation		The deletion of exon(s) 1-11 is a known deleterious mutation.			MCR
		This result is consistent with a diagnosis of Li-Fraumeni syndrome for this individual. Appropriate screening procedures and/or prophylactic measures should be considered. For information regarding the full tumor spectrum and other associated phenotypes, see GeneReviews for this specific gene (http://www.ncbi.nlm.nih.gov/sites/GeneTests/).			
		Since a mutation has been identified, testing of at risk family members is possible.			
		A genetic consultation may be of benefit.			
Caution		CLINICAL CORRELATIONS Test results should be interpreted in context of clinical findings, family history, and other laboratory data. Misinterpretation of results may occur if the information provided is inaccurate or incomplete.			MCR
		TECHNICAL LIMITATIONS Rare polymorphisms exist that could lead to false negative or positive results. If results obtained do not match the clinical findings, additional testing should be considered.			
		Bone marrow transplants from allogenic donors will interfere with testing. Call Mayo Medical Laboratories for instructions for testing patients who have received a bone marrow transplant.			
		EVALUATION TOOLS Multiple in-silico evaluation tools were used to assist in			

Performing Site Legend on Last Page of Report

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* Report times for Mayo performed tests are CST/CDT

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the interpretation of these results. These tools are updated regularly; therefore changes to these algorithms may result in different predictions for a given alteration. Additionally, the predictability of these tools for the determination of pathogenicity is currently unvalidated.

RECLASSIFICATION OF VARIANTS - POLICY
 All detected alterations are evaluated according to ACMG recommendations (Genet Med 2008:10(4):294-300). Variants are classified based on known, predicted, or possible pathogenicity and reported with interpretive comments detailing their potential or known significance. At this time, it is not standard practice for the laboratory to systematically review LIKELY DELETERIOUS alterations or VARIANTS OF UNCERTAIN SIGNIFICANCE that are detected and reported. The laboratory encourages health care providers to contact the laboratory at any time to learn how the status of a particular variant may have changed over time.

TEST CLASSIFICATION
 Laboratory developed test.

Method		MCR
Array comparative genomic hybridization (aCGH) was used to test for the presence of large deletions and/or duplications in the TP53 gene. Mutation nomenclature is based on GenBank accession number NM 000546.4.		
Specimen	Blood	MCR
Reviewed By		MCR
Matthew John Ferber PhD		
Release Date	26 Mar 2013 14:05	MCR

* Performing Site:

MCR	Mayo Clinic Laboratories - Rochester Main Campus 200 First St SW Rochester, MN 55905	Lab Director:
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